019033 ovis aries Q28119 bos taurus Q28116 bos taurus Q91590 ovis aries Q9tqw9 bos indicus	Q9tu21 capra hircu Q95205 ovis aries Q9becO tragulus ja Q9beb9 tragulus ja Q9fme7 arabidopsis	035256 mus musculu Q951r9 macaca fasc 029309 archaeoglob Q9h4q2 homo saplen	Q9c9pu arabidopsis Q91741 xenopus lae Q9v6a0 drosophila	Q9ss03 arabidopsis Q9ckm0 pasteurella Q9m119 arabidopsis	062390 mus musculu 097784 magnaporthe 090774 drosophila 09w5c1 drosophila	035442 mus musculu 046625 bos taurus 09dj12 cowpox viru 09x8t3 streptomyce	P73692 synechocyst Q95530 chlamydia t Q84245 chlamydia t Q928n6 chlamydia p	Q9u416 branchiosto Q9ncp9 branchiosto Q9sit3 arabidopsis	Q13564 homo sapien Q9z1a5 rattus norv Q9nja5 babesia bov	090yi2 fugu rubrip 07557 homo sapien 09und7 homo sapien	O80342 Mus muscutu Q9uhv6 homo sapien Q9pvc9 lepisosteus Q9pvc8 amia calva O98sr8 medalohrama	098sr7 cyprinus ca 098tt4 megalobrama 090283 carassius a 090w27 carassiis a	290%26 carassius a 291%26 amia calva	USIUSE NYPOPHERALM Q90zOl mylopharyng Q90w7 catla Q90w30 cirrhinus m	Q63435 rattus norv Q26765 trypanosoma Q9c1a4 pasteurella	Ogrmq5 acinetobact Ogr620 acinetobact	Q9rbh6 acinetobact Q9rbh4 acinetobact	Q91904 acinetobact Q9f896 acinetobact	necturus m		Q9d813 mus musculu
6.5 53.4 51 6.5 53.4 67 6.5 53.4 73 6.5 53.4 120 6.5 53.4 192	.5 53.4 192 6 .5 53.4 204 6 .5 53.4 217 6 .5 53.4 217 6 46 52.9 1335 10	50.6 227 11 49.4 157 6 49.4 511 17 48.3 113 4	2 48.3 1683 2 48.3 1683 2 48.3 1929	47.1 179 16 47.1 372 10	47.1 554 47.1 631 47.1 707 47.1 711	47.1 1964 11 46.0 134 6 46.0 167 12 46.0 197 2	4 4 4 4 4 4 6 . 0 . 0 . 0 . 0 . 0 . 0 . 0 . 0 . 0 .	46.0 362 5 46.0 364 5 46.0 384 10	46.0 534 4 46.0 534 11 46.0 1292 5	46.0 1822 13 46.0 2023 4 46.0 2023 4	40 46.0 2212 4 40 46.0 2212 4 9.5 45.4 89 13 9.5 45.4 187 13	4 4 4 4 2 4 4 4 4	9.5 45.4 188 13 9.5 45.4 195 13	9.5 45.4 210 13 9.5 45.4 210 13 9.5 45.4 210 13 9.5 45.4 210 13	9.5 45.4 229 11 9.5 45.4 527 5 39 44.8 84 16	44.8 127 2 44.8 127 2	44.8 127 2 44.8 127 2	44.8 127 2 44.8 127 2	44.8 211 13	44.8 278 10 44.8 354 16 44.8 426 16	44.8 450 II
17 18 19 19 20 20 21	Seconds 23 24 24 24 24 25 25 26 26	27 27 30 30	33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3			41 44 44 44 44 44 44	45 46 48 48	49 50 51	52 53 53 54 54	55 56 57	60 60 61	e a printed.		Description 72	nomo sapien	omo sapien omo sapien	omo sapien omo sapien	acaca mula acaca mula acaca mula	cavia porce spalax leuc	mus musculu cavia porce us scrofa	oos taurus
GenCore v	ein search, using sw model July 10, 2002, 08:25:23; Search time 25.06 Secon (without alignments) 110.452 Million cell	US-09-508-054-19 87 1 YLRIVQCRSVEGSCGF 16	GF 16 ext 0.5	222 seqs, 172994929 residues	s satisiying chosen parameters: 55,222 th: 0 th: 2000000000	Minimum Match 0% Maximum Match 100% Listing first 150 summaries	Database : SPTREMBL_19:* 1: Sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* 4: sp_human:* 5: sp_invertebrate:* 6: sp_manman!* 7: sp_mhc:* 9: sp_organel:* 9: sp_phage:* 10: sp_phage:* 11: sp_rodent:* 12: sp_virus:* 13: sp_virus:* 14: sp_uvirus:* 15: sp_uvirus:* 16: sp_hacteriap:* 17: sp_archeap:*	<pre>sp_fungi:* sp_human:* sp_invertebrate:*</pre>	sp_invertebrate:* sp_invertebrate:* sp_inhc:* sp_pranelle:* sp_phage:* sp_plant:* sp_rodent:* sp_rodent:* sp_vertebrate:*		sp_vartebrate:* sp_vertebrate:* sp_unclassified sp_rvirus:* sp_bacteriae:*	유	by analysis of the total score di	\$ Query Match Length DB ID	4 Q9UNL5 4 Q9HBZ1	202 4 014643 217 4 016631 167 4 P78451	199 4 014406 217 4 014407	212 6 Q07368 217 6 Q07367 217 6 Q07369	190 11 070615	59.2 216 11 Q9K2C3 59.2 216 11 Q9JKM4 54.6 217 6 Q28957 Q	Z8 0 Q5NZ04
	OM protein - protein Run on: July	Title: US Perfect score: 87 Sequence: 1	Scoring table: BLG	hed:	Total number of fits sa Minimum DB seq length: Maximum DB seq length:	Post-processing: Min Ma Lis		No. is	Pred. No. is score greater and is derived Result Ques		833	8 8 8 8 8	000	77 77	51.5	13 51.5 59 14 51.5 59 15 47.5 54	40.0				

	PRT; 171 AA.	Created)	Last sequence update	Last annotation upda	
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1	Q9UNL5	-MAY-	01-MAY-2000	01-DEC-2001	
RESULT 09UNL5	60	01	01	01	
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Song H., Peng Y., Dai M., Huang Q., Mao Y., Zhang Q., Mao M., Fu G., Luo M., Chen J., Hu R.;

"Huanan growth hormone variant splitcing gene.";

"Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF110644; AAD48584.1; -.

HSSP; PO1241, 1AXI.

PRINTS; PRO0103; hormone; 2.

PRINTS; PRO0836; SOMATOTROPIN.

PROSITE; PSO0266; SOMATOTROPIN.

PROSITE; PSO0388; SOMATOTROPIN.

SEQUENCE 171 AA: 19801 MW; 9FA9013991FA9F28 CRC64;
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
 GROWTH HORMONE SPLICE VARIANT
                                                                                                                                              Best Local Similarity 93.8
Matches 15; Conservative
                                                                                                                                       1 YLRIVQCRSVEGSCGF 16
      Homo sapiens (Human)
                                SEQUENCE FROM N.A.
TISSUE-PITUITARY;
                      NCBI_TaxID=9606
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099ry3 ephydatia f
099ra3 zymomonas m
09tyk4 caenorhabdi
09fzi4 arabidopsis
0988e4 momordica c
0988e3 momordica c
0988e3 momordica c
0998e3 momordica c
09933 sus scrofa
087909 rahnella aq
09119 neisseria m
054424 serratia ma
054424 serratia ma
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Q9dgh0 brachydanio
Q911s5 mus musculu
Q91vj1 caenorhabdi
Q9suy0 arabidopsis
Q9suy0 arabidopsis
Q9sy0 arabidopsis
Q9sy0 arabidopsis
Q9sy0 arabidopsis
Q9sy0 enturia in
Q95ru6 drosophila
Q95ru6 drosophila
Q96sy9 homo sapien
Q9ug5 komo sapien
Q9ug5 homo sapien
Q9ug5 homo sapien
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Q9lav2 porcine epi
Q9y0b0 mytilus gal
Q9y0a9 mytilus gal
Q9u6u0 mytilus gal
Q9u6u0 mytilus gal
                     Q9s9x4 arabidopsis
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Q01615 pneumocysti
Q91160 oncorhynchu
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Q96vj4 pneumocysti
O94173 pneumocysti
Q06vi1 pneumocysti
Q07242 pneumocysti
Q99vy2 pneumocysti
                                          09ibu7 turkey herp
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           096tu7 venturia na
                           096fcl homo sapien
019780 caenorhabdi
09xu75 caenorhabdi
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O9u8f6 nasonia vit
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Q9urd6 aspergillus
       Q96nx2 homo sapien
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O9f894 acinetobact
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 Q9v5r0 drosophila
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09JRI9
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094423
09DGH0
047239
09HFP0
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Q9TVJ1
Q9SUY0
Q989K1
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Q9P330
Q95RU6
Q9GSY9
Q9UJE1
Q9UJE2
Q9NXG5
Q12960
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Q9U8F6
P87487
Q01615
               Q9V7Q5
Q9S9X4
Q96FC1
Q19780
Q9XU75
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Q9S8E4
Q9S8E3
Q29332
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Q98AH9
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Q9TYK4
Q9FZI4
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Q96VJ4
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Q96VI1
Q07242
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Q9Y0A9
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Q9F894
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Gaps

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95.4%; Score 83; DB 4; Length 171; 93.8%; Pred. No. 2.8e-07; ive 1; Mismatches 0; Indels

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.4%; Score 83; DB 4; Length 179; 93.8%; Pred. No. 2.9e-07; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                     Gu J., Huang Q., Li N., Xu S., Han Z., Fu G., Chen Z.;
"A novel gene expressed in human pituitary.";
submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AF18541, AAG09569.1;
HSSP; P01241; IAXI.
InterPro; IPR001400; SOMATOTROPIN.
Pfam; PF00103; hormone; PR031038; SOMATOTROPIN 2; 1.
SEQUENCE 179 AA; 20561 MW; 0E875A91BE0B9B7E CRC64;
                                                              09HB21;
1-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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014643. 01-5AN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
                                          179 AA
                                          PRT;
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164 FLRIVQCRSVEGSCGF 179
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                                          PRELIMINARY;
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                                                                                                                                                                                         Homo sapiens (Human).
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Best Local Similarity
Matches 15; Conserv
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TISSUE-PITUITARY;
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Gaps

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[1]
SEQUENCE FROM N.A.
MEDLINE=7807151; PubMed=593368;
Shine J., Seeburg P.H., Martial J.A., Baxter J.D., Goodman H.M.;
"Construction and analysis of recombinant DNA for human chorionic
                                                                                                                                                                                                                                                                                                                Homo sapiens (Human),
Wataryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SOMATOMAMMOTROPIN (CHORIONIC SOMATOMAMMOTROPIN) (HCS) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=78160787; PubMed-611657; Seeburg P.H., Shine J., Martial J.A., Ullrich A., Goodman H.M., Baxter J.D.;
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 Score 83; DB 4; Length 217;
Pred. No. 3.5e-07;
1; Mismatches 0; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CHORIONIC SOMATOMAMMOTROPIN CS-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trans. Assoc. Am. Physicians 90:109-116(1977).
EMBL; V00593; CAA23840.1; -.
EMBL; M25118; AAA35721.1; -.
HSSP; P01241; 1A22.
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                                      1; Mismatches
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PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
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Pfam; PF00103; hormone; 1.
95.4%;
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                                                                                                                                                                                                     P78451 PRELIMINARY;
P78451;
01-MAY-1997 (TrEMBLrel. 03,
                                                                                             somatomammotropin.";
Nature 270:494-499(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 92.0
Best Local Similarity 87.5
Matches 14; Conservative
                                      15; Conservative
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 Query Match
Best Local Similarity
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MEDIJINE-983737; PubMed-9709963;
BOGUSZEWSKI C.L., Svensson P.A., Jansson T., Clark R.,
Carlsson L.M.S., Carlsson B.;
"Cloning of two novel growth hormone transcripts expressed in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDILINE=84057143; PubMed=6357679;
MEDILINE=84057143; PubMed=6357679;
Medlman J.P., Hayflick J.S., Vasser M., Seeburg P.H.;
Aln vitro deletional mutagenesis for bacterial production of the 20,000-dalton form of human pituitary growth hormone.";
DAMA 2.183-193(1983).
EMBL; V00520; CAA23779.1; -.
HSSP; P01241; 1HGU.
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MEDLINE-82014939; PubMed-6269091;
DeNoto F.M., Moore D.D., Goodman H.M.;
"Human growth hormone DNA sequence and mRNA structure: possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 83; DB 4; Length 202;
Pred. No. 3.2e-07;
1; Mismatches 0; Indels
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InterPro: IPRO010400; SOMATOTROPIN.
Pfam: PF00103; hormone; 1.
PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00256; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN.2; 1.
SEQUENCE 217 AA; 24803 MW; CCC4D81150D908AC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
38B64D011A9197C6 CRC64;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update) PLACENTAL GROWTH HORMONE 20KDA ISOFORM PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        016631; Q14405;

01.NOV-1996 (TrEMBLrel. 01, Created)

01.NOV-1996 (TrEMBLrel. 01, Last sequence update)

01.DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                      EMBL: AFOOTOMOL. Metab. 83:2878-2885(1998).

EMBL: AFOOTOMOL. AAB71828.1;

HSSP: PO1241; 1A22.

HGAPPO: PRO01400; SOMATOTROPIN.

Pfam: PFO0103; hormone; 2.

PRINTS: PRO0356; SOMATOTROPIN.).

PROSTITE; PSO0266; SOMATOTROPIN.].

PROSTITE; PSO0338; SOMATOTROPIN.].
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Nucleic Acids Res. 9:3719-3730(1981).
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23128 MW;
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Matches 15; Conserv
                                                                                                                                               SEQUENCE FROM N.A.
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Gaps

MEDLINE=89307277; PubMed=2744760;

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Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
"Cloning of four growth hormone/chorionic somatomammotropin-related complementary deoxyribonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta.";
Endocrinology 133:1744-1722(1993).
--- FUNCTION: GROWTH HORMONE PLAYS AN IMPORTANT ROLE IN GROWTH
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                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SOMATOTROPIN 2 PRECURSOR (GROWTH HORMONE 2) (FRAGMENT).
Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SOMATOTROPIN 1 PRECURSOR (GROWTH HORMONE 1).
BAGCAG mulatta (Rhesus maccaque).
Eukaryota; Metazoa; Chordata; Creniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Carcopithecides;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COWTROL.

1- SUBCELLOUAR LOCATION: SECRETED.

1- SUBCELLOUAR LOCATION: SECRETED.

1- SIMILARIY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.

EMBL, 116553; AAA18460.1;

HSSP; P01241; 1AXI.

Interpro, IPR001400; SOMATOTROPIN.

Pfam; PF00103; Hormone: 1.

PRINTS; PR00836; SOMATOTROPIN.

PROSITE; PS00338; SOMATOTROPIN.

PROSITE; PS00338; SOMATOTROPIN.

PROSITE; PS00338; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 77; DB 6; Length 212;
Pred. No. 4.1e-06;
3; Mismatches 0; Indels
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BY SIMILARITY.
27BC91106256E6F5 CRC64;
                                                                                 212 AA.
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                                                                                   PRT;
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MEDLINE-94008724; PubMed-8404617;
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186 BY
210 BY
24525 MW;
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81.2%;
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NON_TER 1 1
SIGNAL <1 ?
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Best Local Similarity 81.2
Matches 13; Conservative
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NCBI_TaxID=9544;
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212 AA;
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TISSUE-PLACENTA;
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Q07368
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Q07367
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Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.,
Seeburg P.H.;
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MEDLINE-89307277; PubMed-2744760;
Chen B.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.
Seeburg P.H.;
                                                                                               ESCUENCE FROM N.A.

MEDLINE=91102558; PubMed=1980158;
Vencak-Jones C.L., Phillips J.A. III.;
Vencak-Jones C. B., Phillips J.A. III.;
Vencak-Jones C. B., Phillips J.A. III.;
Soluting of Alu repeats.";
Science 250:1745-1748 (1990).
EMBL; J03071; AAA52550.1;
HSSP; P01241; 1A22.
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                                "The human growth hormone locus: nucleotide sequence, biology, and evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The human growth hormone locus: nucleotide sequence, biology, and evolution.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 1.1e-06;
2; Mismatches 0; Indels
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Pfam; PF00103; hormone; 1.

PRINTS; PR00836; SOMATOTROPIN.

PROSITE; PS00236; SOMATOTROPIN.1; 1.

PROSITE; PS00338; SOMATOTROPIN.2; 1.

PROSITE; PS00338; SOMATOTROPIN.2; 1.
                                                                                                                                                                                                                                                                                                                          22649 MW; 119656E87AFD55C3 CRC64;
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Last annotation update)
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Pred. No. 1.2e-06;
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Pfam; PF00103; hormone; 2.
PROSITE; PS00338; SOMATOTROPIN_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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87.5%;
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87.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 4:479-497(1989).
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Best Local Similarity 87.5
Matches 14; Conservative
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Best Local Similarity
Matches 14; Conserv
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MEDLINE=20231762; PubMed=10767558; Adkins R.M., Vandeberg J., Li W.H.; "Molecular evolution of growth hormone and receptor in the guinea-pig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99124645; PubMed=9924177; Lioupis A., Nevo E., Wallis M.; Lioupis A., Nevo E., Wallis M.; Lioupis A., Nevo E., Wallis M.; Cloning and characterization of the gene encoding mole rat (Spalax ehrenbergl) growth hormone."; J. Mol. Endocrinol. 22:29-36(1999). EMBL; AJOGS819; CAAO6716.1; -. HSSP; PO1246; 18ST.
                                                                                                                                                                                                                                            Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Spalacinae;
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pfam. PF00103; hormone; 1.
PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00266; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN.1; 1.
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                                                                                                                                  190 AA
                                                                                                                                                                                                                                                                                                                                                                                                          a mammal unresponsive to growth hormone.";
Gene 246:357-363(2000).
EMBL, 8723849; AAF67172.1; -.
HSSP; P01246; 1BST.
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Pfam; PF00103; hormone; 1.
PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00266; SOMATOTROPIN. 1; PROSITE; PS00338; SOMATOTROPIN. 1; 1.
                                                                                                                                  PRT;
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                         Query Match
Best Local Similarity 58.8
Matches 10; Conservative
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     1 YLRIVQCRSVEGSCGF 16
                                                                                                                                  PRELIMINARY;
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"Cloning of four growth hormone/chorionic somatomammotropin-related complementary deoxytibonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta.";
Endocrinology 133:1744-1722(1993).
-!- FUNCTION: GROWTH HORMONE PLAYS AN IMPORTANT ROLE IN GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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Endocrinology 133:1744-1752(1993).
-!- FUNCTION: GROWTH HORMONE PLAYS AN IMPORTANT ROLE IN GROWTH
                                                   -!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
EMBL; L16552; AAA1839.1; -.
INTERPRO. 101241; 1AAI.
InterPro; IPR01400; SOMATOTROPIN.
PAGMI; PR01013; hormone; 1.
PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN.2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: SECRETED.
-!- SIMILARITY: BELONGS TO THE SOMATOTROPIN/PROLACTIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                  Score 77; DB 6; Length 217;
Pred. No. 4.2e-06;
3; Mismatches 0; Indels
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BY SIMILARITY.
FIEBGAFDBBA1B185 CRC64;
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BY SIMILARITY.

FF5AA8915131F2BC CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SOMATOTROPIN 3 PRECURSOR (GROWTH HORMONE 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 AA.
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PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
                                                                                                                                                                                                                                            SOMATOTROPIN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPR001400; SOMATOTROPIN. Pfam; PF00103; hormone; 1. PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-PLACENTA; MEDLINE-94008724; PubMed-8404617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24874 MW;
                                                                                                                                                                                                                                                                                                24942 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L16554; AAA18841.1; -. HSSP; P01241; 1AXI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.5%;
81.2%;
                                                                                                                                                                                                                                                                                                                                                      88.5%;
81.2%;
                                                                                                                                                                                                          Pituitary; Hormone; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 81.2°
.....hos 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 88.5
Best Local Similarity 81.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                             1 YLRIVQCRSVEGSCGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                             208 2
217 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                             DISULFID
SEQUENCE .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               007369;
                                                                                                                                                                                                                           SIGNAL
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Qi S.-z., Wang X.-z., Zhou S.-w., Jia F., Wang H.-y., Xia, Li, Li J.; "cDNA sequence og the porcine growth hormone."; Chin. J. Biotechnol. 5:35-39(1989).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostoml;
Sus.
                                                                                                                 Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 217;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases.
                                              GROWTH HORMONE.
45996BE119B08DD3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24470 MW; F708195D8A678831 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Sulna; Suldae;
                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GROWTH HORMONE (FRAGMENT).
                                                                                                                 11;
                                                                                                                                             3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.6%; Score 47.5; DB 6; 58.8%; Pred. No. 0.92; Live 2; Mismatches 4;
                                                                                                               Score 51.5; DB
Pred. No. 0.17;
3; Mismatches
                                                                                                                                                                                                                                                                                           217 AA
   PS00338; SOMATOTROPIN_2; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 AA.
                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0836; SOMATOTROPIN.
PROSTTE; PS00266; SOMATOTROPIN.
SEQUENCE 217 AA; 24470 MW: F7001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001400; SOMATOTROPIN. Pfam; PF00103; hormone; 1.
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Μ.
                                                                                                               59.2%;
58.8%;
                               26
216
24822 N
                                                                                                                                                                                                             200 YLRVMKCRRFVESSCAF 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 YLRAMKCRRFVESSCAF 217
                                                                                                              Query Match 59.2
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                               1 YLRIVQCRS-VEGSCGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1995) to the EMBL; U19787; AAA73477.1; HSSP; P01246; 1BST.
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Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                               1
27
216 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-PITUITARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-PITUITARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                          GROWTH HORMONE
   PROSITE;
                                                                  SEQUENCE
                                   SIGNAL
                  Signal.
                                                                                                                                                                                                                                                                                                          028957;
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                                                                                                                                                                                                                                                                                           028957
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                                                  CHAIN
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Q28957
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                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nguyen T.N.K., Liebhaber S.A.; "Mouse Growth Hormone Locus: Nucleotide Sequence and Phylogenetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cavia porcellus (Guinea pig).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NCBI_TaxID=10141;
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                                                               Length 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; DB 11; Length 216; 0.17;
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SEQUENCE FROM N.A.

COGOTICO D.M., Fuller P.J., Herington A.C.;

CLOINING and Sequence of guinea pig growth hormone (GH).";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF233853; AAF36409.1; -

HSSP; P01246; 1BST.

InterPro; IPR001400; SOMATOTROPIN.

Ffam; PF00103; hormone; 1.

PRINTS; PR00186; SOMATOTROPIN.

PROSITE; PS00266; SOMATOTROPIN.1; 1.
                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001400; SONATOTROPIN.
Pfam; PF00103; hormone; 1.
PRINTS; PR008056; SONATOTROPIN., 1.
PROSITE; PS00366; SONATOTROPIN., 1; 1.
PROSITE; PS00338; SONATOTROPIN., 2; 1.
SEQUENCE 216 AA; 24682 MW; FC2A05DA02536B18 CRC64;
               EEABBA523BA0ADFE CRC64;
                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GROWTH HORMONE PRECURSOR.
                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
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α
                                                               Score 51.5; DB Pred. No. 0.17;
 GROWTH HORMONE
                                                                                                                                                                                                                                             216 AA
                                                                                               3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51.5;
Pred. No. 0.
                                                                                                                                                                                                                                             PRT;
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               24627 MW;
                                                             59.2%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.2%;
                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                           200 YLRVMKCRRFVESSCAF 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-1995) to th
EMBL; U34362; AAC99988.1;
HSSP; P01246; 1BST.
                                                                                                                             1 YLRIVQCRS-VEGSCGF 16
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                                                                                             10; Conservative
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Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                           PRELIMINARY;
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27 :
216 AA;
                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        GROWTH HORMOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Analyses.";
               SEQUENCE
                                                             Query Match
                                                                                                                                                                                                          RESULT 13
Q9R2C3
                                                                                                                                                                                                                                           Q9R2C3
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Q9JKM4
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SEQUENCE FROM N.A.
MEDLINE-87204193; Pubmed=3472230;
Hampson R.K., Rottman F.M.;
Hampson R.K., Rottman F.M.;
Hampson R.K., Rottman F.M.;
Hampson R.K., Rottman F.M.;
The final intron predicts a high molecular weight variant of bovine the final intron predicts a high molecular weight variant of bovine "."

" A B 84:2673-2677(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chikuni K., Nagatsuma T., Tabata T., Monma M., Saito M., Ozawa S., Ozutsumi K.;
"Genetic variants of the growth hormone gene in Japanese cattle.";
Anim. Sci. Technol. 65:340-346(1994).
EMBL: D30713; BAA06379.1; -.
HSSP; P01246; 1BST.
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MEDLINE-83116949; PubMed-6296767;
Woychik R.P., Camper S.A., Lyons R.H., Horowitz S., Goodwin E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning and nucleotide sequencing of the bovine growth hormone gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53.4%; Score 46.5; DB 6; Length 67; 52.9%; Pred. No. 0.44; ive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 73;
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M -> T (IN REF. 1).
95D6485BEEECD3BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER 1 1 SEQUENCE 67 AA; 7793 MW; 757AA5D81CDE2CC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GROWTH HORMONE C VARIANT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 84:2673-2677(1987).
EMBL, M16253; AAA30547.1; -.
HSSP; P01246; 1BST.
InterPro; IPR001400; SOMATOTROPIN.
Pfam; PF00103; hormone; 1.
PRINTS; PR00136; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 10:7197:7210(1982)
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Pfam; PF00103; hormone; 1.
PRINTS: PR00836; SOMATOTROPIN_2; 1.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
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73 AA; 8468 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YLRIVQCRSV-EGSCGF 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
  Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9913;
                        NCBI_TaxID=9913;
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SEQUENCE
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Q28116
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-00V-1996 (TrEMBLrel. 01, Last sequence update)
01-00V-2001 (TrEMBLrel. 17, Last annotation update)
01-00V-1996 (TREMBLROL. 17, Last annotation update)
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Lagziel A., Soller M.;
"DNA sequence of SSCP haplotypes at the bovine growth hormone (bGH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ofir R., Gootwine E.; "Sequence analysis of the GH1, GH2-N and GH2-Z copies of the ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; mammalia; Eutheria; Cetartiodactyla; Ruminantla; Pecora; Bovoidea; Bovidae; Caprinae; Ovis.
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Pred. No. 0.33;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                            6; Length 28;
                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                               NON_TER 1 1 1 SEQUENCE 28 AA; 3397 MW; 39B00CE59B01B926 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE 51 AA; 6083 MW; 7358BBC165696B23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
GROWTH HORMONE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                         53.4%; Score 46.5; DB 52.9%; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 AA
                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                      Anim. Genet. 0:0-0(1999).

EMBL, AF117350; AAF28806.1; -.
HSSP, P01246; 1BST.

InterPro: IPR001400; SOMATOTROPIN.

Pfam; PF00103; hormone; 1.

PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  growth hormone gene.";
Mamm. Genome 0:0-0(1997).
EMBL; AF002117; AAB64117.1; -.
HSSP; P01246; 1BST.
INTERPO: IPR001400; SOMATOTROPIN.
Pfam; PF00103; hormone; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.48;
52.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YLRIVQCRSV-EGSCGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 YLRVMKCRRFGEASCAF 51
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YLRIVQCRSV-EGSCGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 YLRVMKCRRFGEASCAF 28
                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 9; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               019033;
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019033
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028119
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MEDLINE-97050633; PubMed-8895361;
MEDLINE-97050633; PubMed-8895361;
Lacroix M.C., Devinoy E., Servely J.L., Pulssant C., Kann G.;
"Expression of the growth hormone gene in ovine placenta: detection and cellular localization of the protein.";
Endocrinology 137:4886-4892(1996).
EMBL: U49063; AAC48679.1;
                                                                                                                                                                                                                                                                                                                                                                                                     Capra hirous (Goat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Capra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Caprinae, Ovis.
                                                                           6; Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN=INDIAN BEETAL;
A Mukhopadhyay U.K., Sahni G.;
A mindian goat growth hormone cDNA.";
L submitted (AuG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF17287; AAF03130.1; -.
R HSSP, P01246; 1BST.
R InterPro; IPR001400; SOMATOTROPIN.
R PRINTS; PR00836; SOMATOTROPIN.
R PROSITE; PS00236; SOMATOTROPIN.1; 1.
R PROSITE; PS00336; SOMATOTROPIN.2; 1.
SEQUENCE 192 AA; 21977 MW; A5A6977B607F31BA CRC64;
                                                                                                                 Indels
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PROSITE; PS00338; SOMATOTROPIN_2; 1.
SEQUENCE 192 AA; 21947 MW; 0C7B5EAF606B3ECC CRC64;
                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GROWTH HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                       Score 46.5; DB
Pred. No. 1.2;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.4%; Score 46.5; DB
52.9%; Pred. No. 1.2;
iive 3; Mismatches
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                                                                                                                                                                                                                                                                                           PRT;
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                                                                           53.4%;
                                                                                                                                                                           176 YLRVMKCRRFGEASCAF 192
                                                                                                                                                     1 YLRIVQCRSV-EGSCGF 16
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                                                                         Query Match 53.4
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              095205;
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Q95205
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   SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Ofir R., Gootwhole E.;

Ofir R., Gootwho E.;

"Sequence analysis of the GH1, GH2-N and GH2-Z copies of the ovine growth hormone gene.";

Mamm. Genome 0:0-0(1997).

EMBL; AF002120; AAB64120.1; -.

HSSP; P01246; 1BST.
                                                                                                                                                                                                                                                                                 Ovis aries (Sheep).

Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprine; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos indicus (Zebu), and
Bubalus bubalis (Domestic water buffalo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-INDIAN;
A Mukhopadhyay U.K., Sahni G.;
A Mukhopadhyay U.K., Sahni G.;
Mukhopadhyay U.K., Sahni G.;
Submitted (AuG.1999) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF177289; AAF03132.1; -.
R HSSP; P01246; LBST.
R INCEPPO; IPR001400; SOMATOTROPIN.
R Pfam; PF00103; hormone; 1.
R Pfam; PF00103; SOMATOTROPIN.
R PRINTS; PR00836; SOMATOTROPIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                     O9TSG0;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.4%; Score 46.5; DB 52.9%; Pred. No. 0.78; iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 AA.
                                                                                                                                                     120 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001400; SOMATOTROPIN.
Pfam; PF00103; hormones; 1.
PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                 GROWTH HORMONE (FRAGMENT).
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                                         1 YLRIVQCRSV-EGSCGF 16
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                                                                                                                                                     PRELIMINARY;
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NCBI_TaxID=9915, 89462;
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ROMANOV;
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Tabata S.;
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"Molecular evolution of growth hormone (GH) in Cetartiodactyla:
Cloning and characterization of the gene encoding GH from a primitive
ruminant, the chevrotain (Tragulus javanicus).";
Gen. Comp. Endocrinol. 123:6-72(2001).
EMBL; AJ309713; CAC29336.1;
HSSP; P01246; 1BST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
Tragulidae; Tragulus.
                                                                                                                                                                                                                                                                                                                                                          4; Indels 1;
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                                                                                                                                                                                                                                                                                            Length 204;
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GROWTH HORMONE.
2003E44372EA7BDE CRC64;
                                                                                                                                                                         NON_TER 1 1 SEQUENCE 204 AA; 23462 MW; EBBB9451892635C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-57N-2001 (TrEMBLrel. 17, Created)
01-57N-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Pred. No. 1.4;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                               9;
                                                                                                                                                                                                                                                                                         Score 46.5; DB (Pred. No. 1.3; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tragulus javanicus (Lesser Malay chevrotain).
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                     Interpro; IPR001400; SOMATOTROPIN.
Pfam; PF00103; hormone; 1.
PRINTS; PR00836; SOMATOTROPIN.
PROSTIE; PS00266; SOMATOTROPIN.
PROSTIE; PS00338; SOMATOTROPIN.1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR001400; SOMATOTROPIN.
Pfam: PF00103; hormone; 1
PRINTS; PR00836; SOMATOTROPIN.
PROSITE; PS00256; SOMATOTROPIN. 1:
PROSITE; PS00338; SOMATOTROPIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21434966; PubMed-11551118;
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52.98;
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Best Local Similarity 52.9%;
Matches 9; Conservative
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Best Local Similarity 52.3%,
Best Local Similarity 52.3%,
Conservative
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28
217 AA;
HSSP; P01246; 1BST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-LIVER,
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SEQUENCE
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Q9BEC0
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"Molecular evolution of growth hormone (GH) in Cetartiodactyla:
"Molecular evolution of growth hormone (GH) in Cetartiodactyla:
Cloning and characterization of the gene encoding GH from a primitive
ruminant, the chevrotain (Tragulus javanicus).";
Gen. Comp. Endocrinol. 123:62-72(2001).
GENBL, A3109144; CAC29337.1;
INTERPRO 1PRO01400; SOMATOTROPIN.
PRSP: P01246; IBST.
INTERPRO; PRO0103; hormone: 1.
PROSITE; PS00036; SOMATOTROPIN.
PROSITE; PS00036; SOMATOTROPIN.]; 1.
PROSITE; PS00038; SOMATOTROPIN.]; 1.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
NINESIN-LIKE PROFEL.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 5. III.
Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones.";
DNA Res. 4:401-414(1997).
EMBI: AB008269; BAB10642.1; -.
HSSP; P17119; 3KAR.
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Tragulus javanicus (Lesser Malay chevrotain).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
Tragulidae; Tragulus.
NCBI_TaxID=9849;
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MEDLINE=98162728; PubMed=9501997;
Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima
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Pred. No. 10;
2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3B89CCFA72EA7BDE CRC64;
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Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                   MEDLINE-21434966; PubMed-11551118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001752; kinesin.
Pfam; PF00225; kinesin; 1.
PRINTS; PR00380; KINESINHEAVY.
SMART; SM00129; KISC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24635 MW;
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70.0%;
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Best Local Similarity 52.5.
Fra 9; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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217 AA;
                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE=LIVER;
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Gaps

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4; Indels

511 AA.

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TISSUE=TESTIS;
Hashimoto K., Osada N., Hida M., Kusuda J., Tanuma R., Hirai M.,
                                                                                                                                                                                                                                                                                                                                               Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
                                                                                                                                          Score 43; DB 6; Length 157;
Pred. No. 4.4;
                                                                                                                                                                                                                                                                                       01-0AN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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50.08;
                                                                                                                                          Query Match
Best Local Similarity 61.5%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                          GLUTAMATE SYNTHASE (GLTB).
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Best Local Similarity 50.0°
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          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                               Lin J., Poole J., Linzer D.I.;
"Three new members of the mouse prolactin/growth hormone family are homologous to proteins expressed in the rat.";
Endocrinology 138:5541-5549(1997).
                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                 Muller H., Ishimura R., Orwig K.E., Liu B., Soares M.J.; Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CS7BL/6J;
Lin J., Poole J., Linzer D.I.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF015562; AAB68824.1;
EMBL; AF011383; AAB68299.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROLACTIN-LIKE PROTEIN-A. 585B2731DCED57B6 CRC64;
                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PROLACTIN-LIKE PROTEIN A PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 17.5 KDA PROTEIN.
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PROSITE; PS00266; SOMATOTROPIN_1; 1.
PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
                                                                                     227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Mismatches
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                                                                                                           Created)
                                                                                     PRT;
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InterPro; IPR001400; SOMATOTROPIN.
                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J;
MEDLINE=98049410; PubMed=9389542;
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227 PR
26336 MW;
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01-JAN-1998 (TrEMBLrel. 05
01-JUN-2001 (TrEMBLrel. 17
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                                                                                     PRELIMINARY;
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NCBI_TaxID=9541;
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                             1074 QCRATKGSCG 1083
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        6 QCRSVEGSCG 15
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                                                                                  035256
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Q95LR9;
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035256
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Q95LR9
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PEDLINE-98049343; PubMed=9889475;
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MEDKINE-98049343; PubMed=9889475;
MEDKINE-98049343; PubMed=9889475;
MEDKINE-98049343; PubMed=9889475;
MECHANT K.A., Dodson R.J., Graham D.E., Kyrpides N.C.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Richardson D.L., Merlavage A.R., McKenney K., Adams M.D., Loftus B.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Overbeek R., Gocayne J.D., Meidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea R.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Mature 390:364-370(1997).
EMBL; AE001038; AAB90287.1; -.
HSSP; P55907; IXER.
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InterPro: JPR003009; FWN.enzyme.
InterPro: JPR002932; Glu_synthase.
Pfam: PF006437; fer44; 2.
Pfam: PF01645; Glu_synthase: J.
PROSTIF: PS00198; 4Fe4S_FERREDOXIN; 2.
Hypothetical protein; Iron-sulfur; Complete protecome.
SEQUENCE 511 AA; 56203 MW; 0FA661F793D6983F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7
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TISSUE=LIVER;
MEDLINE=96186527; PubMed=8606056;
InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1683 AA; 189707 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.3%;
53.3%;
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1039 YLRILQFKKADGSYG 1053
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                           195 ECLSSHGSCGF 205
                                                                                                                                                                                                                                                                                                                  6 QCRSVEGSCGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 32
Q91741
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 DAR DAR DAR SE
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REPUBLICE TO COLUMBIA.

REPUBLICE A. COLUMBIA.

RATIN-CV. COLUMBIA.

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA WILL O., Alonso J., Chen H., Cheuk R.F., Chin C.W.,

Ra Buehler E., Chan A., Chao Q., Chen H., Creuk R.F., Chin C.W.,

Ra Buehler E., Chan A., Chao Q., Chen H., Creuk R.F., Chin C.W.,

Ra Buther J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,

Ra Hunter J.L., Jenkins J., Johnson Hopson C., Khan S., Khaykin E.,

Ra Langin-Hooper S., Lee A., Lee J.W., Lenz C.A., Li J. H., Li Y.-P.,

Ra Lin X., Liu S.X., Liu Z.A., Luros J.S., Matti R., Marziali A.,

Ra Lin X., Liu S.X., Liu Z.A., Liu Z.A., Miltson W.C., Osborne B.I.,

Ra Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Ra And G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Ra Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Ru Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

Ru Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

Ra Haliana.,

Ra Ha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudlootyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                 Homo sapiens (Human).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Prohlich O., Po C., Young L.G.;
"Genomic organization of the human epididymal EP2 gene and its
"Genomic organization of the human epididymal EP2 gene and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 113;
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                                                                                                                                                                                                                                                                                                                           relationship differential openes.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY003129; AAG21880.1;
InterPro; IPR001230; PRENYLA.
PROSITE; PS00294; PRENYLATION; UNKNOWN.1.
SEQUENCE 113 AA; 12686 MW; F962A417664352A3 CRC64;
                                                                                                      01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42; DB 4;
Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1286 AA.
                                                                       113 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 408:816-820(2000).
EMBL; AC013288; AAG60067.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                       PRELIMINARY;
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Best Local Similarity
Matches 7; Conserv
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01-JUN-2001
                                                                     Q9H4Q2
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Q9C9P0
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                                  RESULT 30
                                                   Q9H4Q2
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Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO R., Kato Y., Nondaw M., Nakayama K., Takahashi M.;

Mo R., Kato Y., Nondaw M., Nakayama K., Takahashi M.;

Innkage analysis of the frog MHC.";

Immunogenetics of the frog MHC.";

Immunogenetics BAA11188.1;

IEMBL; D78001; BAA11188.1;

InterPro; IPR00124; 1129.

InterPro; IPR001599; Alpha_2_macroglobin.

InterPro; IPR001640; Anaphylatoxin.

InterPro; IPR001134; Netrin_C.
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69;
                                                                                                                                                                                                                                                                                                   DB 10; Length 1286;
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                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                          DE17E1118FDB7BCA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
FOURTH COMPONENT OF COMPLEMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS00477; ALPHA_2_MACROGLOBULIN; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 ;
                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                   Score 42; DB 1
Pred. No. 53;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1683 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                            PROSITE; PSO0107; PROTEIN KINASE_ATP; 1.
PROSITE; PSS0011; PROTEIN KINASE_DOM; 1.
Transferase: Transferase: SEQUENCE 1286 AA; 143488 MW; DE17E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00207; A2M; 1.
Pfam; PF01835; A2M_N; 1.
Pfam; PF01821; ANATO; 1.
Pfam; PF01759; NTR; 1.
PRIWTS; PR00004; ANAPHYLATOXN.
ProDom; PD003264; Anaphylatoxin; 1.
SWART; SM00104; ANATO; 1.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
SMART; SM00220; S_TKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01178; ANAPHYLATOXIN_2;
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333

RESULT

Created)

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Q9CKMO;
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Q9CKM0
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RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,

Amanatides D.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.E.,

B. Gocaye R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Bratton G.G., Wortnam J.R., An H.-J., Andrews-Fenantwoch C., Raldwin D.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

Abril J.E., Agbayani A., An H.-J., Andrews-Fenantwoch C.R., Miklos G.L.G.,

RA Ballew R.M., Basu M., Barandale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu M., Barandale J., Bayraktaroglu L., Beasley E.M.,

Baltew R.M., Basu D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Borkova D., Botcham M.R., Bouck J., Brokstein P., Brottler P.,

Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Burtis R.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Borkova D., Botchen A.R., Dang Z., Mays A.D., Dew I., Dietz S.M.,

Bortis R.O., Bornell J.H., Gu Z., Guan P., Berris B., Davis B.C.,

RA Hartis N.J., Evangelista C.C., Ferraz C., Ferrieca S., Fleischmann W.,

RA Hartis N.L., Harvy D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hartis N.L., Harvy D., Heiman T.J., Hernandez J.R., Mocheck A.,

Jalali M., Kallsh F., Karpen G.H., Ne. Z., Kennison J.A.,

RA Hartis N.L., Harvy D., Heiman T.J., Milang J., Linag Y., Lin X.,

Markluo G. Milshina N.V., Mobarry C., Morris S., Kulp D., Lai Z.,

Ra Brackloo G. Milshina N.V., Mobarry C., Morris J. Wolphrer E., Shan H.,

Shue B.C., Siden-Klamos I., Simpson M., Strong R., Pacleb J.M.,

Ra Spier E., Spradling A.C., Stapleton M., Strong S., Yao Q.A.,

Nang Z.-Y., Wassarman D.A., Weinsteon B., Wall S., Rang S., Zhao Q., Zhao Q., Zhao G., Zhao S., Zhao S., Zhao G., Siden-Klamos G., Shao R., Worley S., Wulliams S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_Tax.D=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FBgn0033718; CG13162.
1929 AA; 219961 MW; A409187CC6AECA66 CRC64;
                                                                                              Last sequence update)
Last annotation update)
                        1929 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1036 AA.
                                                                        Created)
                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                        PRT;
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EMBL; AE003822; AAF58528.1;
                                                                01-MAY 2000 (TrEMBLrel. 13, 01-MAY 2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14, CG13162 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity bo...
                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
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                                               Q9V6A0;
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                   Q9V6A0
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                                                                                                                Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Nall. Acad. Sci. U.S.A. 98:3460-3465(2001).
BMBL, AE006197; AAK03661; --
HSSP, Q45560; IBWE.
InterPro: IPR001455; QtC_heme_bind.
Pfam; PF00037; fer4; 3.
PROSTIE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SEQUENCE 179 AA; 20170 MW; AEGCIEI748FA4653 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pasteurella multocida.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOF250E6BEE250CF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 41.5; DB
Pred. No. 53;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000767; Disease_resist.
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
InterPro; IPR000157; TIR.
Pfam; PF00560; LRR; 3.
Pfam; PF00931; NB-ARC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-PM70;
MEDLINE-21145866; Pubmed-11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pfam; PP01582; TIR; I.
SMRNTS; PR00364; DISEASERSIST.
SWART: SW00255; TIR; II.8944 MW;
47.78;
47.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      863 YLKVVNCESLERLDCSF 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YLRIVQCRSVEG-SCGF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                             F12P19.1 PROTEIN. F12P19.1.
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Gaps

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Q9M1L9

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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
61-0CT-2001 (TrEMBLrel. 18, Last annotation update)
62:BACR7A4.15 PROTEIN.
62:BACR7A4.15 OR CG3703.
Drosophila melanogaster (Fruit fly).
64:Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
65:Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
64:Pterygota Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Papagiannakis G., Spanos L., Bolshakov V., Siden-Klamos I., Louis C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=4091-5-8;
MEDLINE=99452735; PubMed=10521529;
DeZwaan T.M., Carroll A.M., Valent B., Sweigard J.A.;
"Magnaporthe grisea Pthlip is a novel plasma membrane protein that
mediates appressorium differentiation in response to inductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
                                                                                                                                                                                                                                                                                                                                  Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.1%; Score 41; DB 3; Length 631; 47.6%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  substrate cues.";
Plant Cell 11:2013-2030(1999).
EMBL; AFI19670; AAD30436.1; -.
SFOUENCE 631 AA; 69349 MW; B7F377C417635279 CRC64;
                                                                                                                                                                                                                     ANK repeat; Repeat.
SEQUENCE 554 AA; 58351 MW; 5E59375C5353BCOF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                  Score 41; DB 11;
Pred. No. 35;
1; Mismatches 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               707 AA
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                                                                                                                                                           PROSITE; PS50088; ANK_REPEAT; 5.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
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                                                                                                                                                                                                                                                                                                                                    47.18;
70.08;
                    MGD; MGI:107471; Notch4.
InterPro; IPR002110; ANK.
Pfam; PF00023; ank; 6.
PRINTS; PR01415; ANKYEIN.
SMART; SM00248; ANK; 5.
                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 70.0
نمر 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :||| ||||
465 RCRSRSGSCG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                              6 QCRSVEGSCG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=148305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9Y784
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Q9NF74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 38
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DR DR DR SO S
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EMBL: U48691; AAC52631.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                 Gaps
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Was musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinee; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R., WebchSelgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer K.P.X., Quetier F., Salanoubat M.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 24;
                       DB 16; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL138654; CAB86673.1;
InterPro; IRR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 4.
SMART; SM00343; ZnF_C2BC; 4.
Hypochetical protein; Zinc-finger.
SEQUENCE 372 AA; 39913 WW; 66E39D42E5E3FID2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 39.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   554 AA.
                                                                                                                                                                                                                                                                                                                                    372 AA
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                                                                               Mismatches
                          Score 41;
                                                    Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE-96281668; PubMed-8681805;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.18;
                    47.18;
58.38;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
                                           Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
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                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                   : (:||| | ||
117 KAVECRSCEDSC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :| ||||||
189 RCPVFEGSCGF 199
                                                                                                                                3 RIVQCRSVEGSC 14
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Gaps

RESULT 37 Q62390

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01-JAN-1998 (
01-JAN-1998 (
01-DEC-2001 (
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035442
      RA RA RA RA DR RL DR DR DR DR SQ
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                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              EG:BACRTAA.15 OR CG3703.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                            Gaps
"Sequencing the distal X chromosome of Drosophila melanogaster."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                          ö
                                                                                                                                                                                             Length 707;
                                                                                                                                                                                                                          4; Indels
                                                          Benos P.; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AL109630; CAB51686.1; -. FlyBase; FBgn0040348; EG:BACR7A4.15. InterPro; IPR004012; Run.
                                                                                                                                                  5D78E6A8E2432B06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                               Score 41; DB 5;
                                                                                                                                                                                                                                                                                                                                                              711 AA.
                                                                                                                                                                                                           Pred. No. 45;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Created)
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                                                                                                                               PF02759; RUN; 1.
                                                                                                                                                                                             47.18;
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Best Local Similarity 40.0.
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266 FIAFLQCDAIEGSVG 280
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                                                                                                                                                                                                                                                      1 YLRIVQCRSVEGSCG 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                            SEQUENCE FROM N.A.
                                                                                                                                                SEQUENCE
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                                                                                                                                      Pfam;
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Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Glubs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Rower L., Mahaliras G., Qln S., Ahearn M.E., Dankers C., Lasky S., Rower L., Mahaliras G., Qln S., Traicoff R., Zackrone K., Hood L.; "Sequence of the mouse major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                              5; Length 711;
                                                                                                                                                                                                                                                                                                                              4; Indels
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                                                                                                                                                                                                          78612 MW; B8547DA2ABA1779F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1964 AA
                                                                                                                                                                                                                                                                              Score 41; DB
Pred. No. 45;
                                                                                                                                                                                                                                                                                                                            5; Mismatches
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PROSITE; PS500897; ANK_REPEGION; 1.
PROSITE; PS000010; ASX_HERPEGION; 1.1
PROSITE; PS00002; EGF_1; UNKNOWN_28.
PROSITE; PS01186; EGF_2; 21.
PROSITE; PS01187; EGF_CA; 9.
PROSITE; PS01087; EGF_CA; 9.
                                                                                                            EMBL: AE003419; AAF45572.1; -.
FlyBase; EBgn0040348; EG:BACK7A4.15.
InterPro; IPR004012; Run.
PF02759; Run; 1.
SEQUENCE 711 AA; 78612 MW; B8547
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EGF-like.
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Mammalia; Eutheria; Rodentia;
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SMART; SM00179; EGF_CA; 12.
SMART; SM00001; EGF_IIke; 14.
SMART; SM00004; NL; 2.
                                                                                                                                                                                                                                                                              47.18;
40.08;
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EGF_Ca.
EGF_II.
Notch.
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Pfam; PF00023; ank; 6.
Pfam; PF00008; EGF; 27.
Pfam; PF00066; notch; 2.
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HSSP; P08709; 1BF9.
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PRINTS; PR00010; EGFBLOOD
PRINTS; PR01452; NOTCH.
                                                                                                                                                                                                                                                                                                                            6; Conservative
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270 FIAFLQCDAIEGSVG 284
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SEQUENCE 1964 AA; 2
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InterPro; IPR000561;
InterPro; IPR000742;
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InterPro; IPR001438;
InterPro; IPR000800;
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Best Local Similarity
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PRT;
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                                                                  110 LRDAQCPGVKKCCEGSCG 127
                                                  2 LRIVQCRSV----EGSCG 15
                          Conservative
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              Similarity
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                         10;
  Query Match
              Best Local
Matches 1
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MEDLINE-93280175; PubMed=7685029;
MIDLINE-93280175; PubMed=7685029;
Molhulzen H.O., Alkemade H.A., Zeeuwen P.L., de Jongh G.J.,
Wieringa B., Schalkwijk J.;
Mieringa B., Schalkwijk J.;
Inhibitor from Cultured Human Keratinocytes
"SKALP/Flaffin: An Elastase Inhibitor from Cultured Human Keratinocytes
Purification, cDNA Sequence, and Evidence for Transglutaminase Cross-
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tamechika I., Itakura M., Saruta Y., Furukawa M., Kato A., Tachibana S., Hirose S.; "Accelerated evolution in inhibitor domains of porcine elafin family
                                                                                                                                                                                                                                                                                                                                                                                                               Zeeuwen P.L., Hendriks W., de Jong W.W., Schalkwijk J.; indentification and Sequence Analysis of Two New Members of the SKALP/elafin and SPAI-2 Gene Family; Blochemical Properties of the Transglutaminase Substrate Motif and Suggestions for a New
                                                                                                                                                                                                                  BTRAPPIN-2.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                          ó;
 Score 41; DB 11; Length 1964;
Pred. No. 1.2e+02;
1; Mismatches 2; Indels C
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Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                            01-JUN-1998 (TrEMBLE-1. 06, Last sequence update)
01-DEC-2001 (TrEMBLE-1. 19, Last annotation update)
BTRAPPIN-2 PROTEIN (FRAGMENT).
                                                                                                                                            134 AA
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PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
PROSITE; PS00313; SVP_I; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 268:12028-12032(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nomenclature.";
J. Biol. Chem. 272:20471-20478(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            members.";
J. Biol. Chem. 271:7012-7018(1996).
EMBL; A223216; CAA11184.1;
HSSP; P19957; 2REL.
Interpro; IPR000737; Squash.
Interpro; IPR002098; SVP. I
                                                                                                                                                                  Created)
                                                                                                                                          PRT;
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MEDLINE=96215132; PubMed=8636131;
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MEDLINE=97400522; PubMed=9252357;
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PRINTS; PR00003; 4DISULPHCORE.
PRINTS; PR00293; SQUASHINHBTR.
ProDom; PD001224; WAP; 1.
 47.18;
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01-JUN-1998 (TrEMBLrel. 06,
                          Conservative
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                    Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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1875 RCRSRSGSCG 1884
Query Match
Best Local Similarity
Matches 7; Conserv
                                                    6 OCRSVEGSCG 15
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
NCBI_TaxID=10243;
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Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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STRAIN=ELEPHANTPOX;
STRAIN=20569533; PubMed=11119592;
Saraiva M., Alcami A.;
"CrmE, a novel soluble tumour necrosis factor receptor encoded by Poxviruses.";
J. Virol. 75:226-233(2001).
EMBL; AJ272008; CAC15562.1; --.
HSSP; P19438; LEXT.
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                                      4.
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Pred. No. 16;
0; Mismatches 7; Indels
 Length 134;
                                      Indels
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SEQUENCE FROM N.A.
STRAIN=A3(2);
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=A3(2);
Oliver K., Harris D.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 20.3 KDA PROTEIN.
                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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46.0%; Score 40; DB
55.6%; Pred. No. 13;
Live 0; Mismatches
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Pfam; PF00020; TNFR_c6; 2.

ProDom; PD000711; TNFR_c6; 1.

SMART; SM00208; TNFR; 3.

PROSITE; PS00623; TNFR_NGFR_1; UNKNOWN_1.

PROSITE; PS00509; TNFR_NGFR_2; 2.

SEQUENCE 167 AA; 18500 MM; FB790E79276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 46.0%; Score 40; Best Local Similarity 53.3%; Pred. No. 1 Matches 8; Conservative 0; Mismatch
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Gaps

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Bannantine J.P., Rockey D.D.,
"Use of primate model system to identify Chlamydia trachomatis protein
antigens recognized uniquely in the context of infection.";
Microbiology 145:207-2085(1999).
EMBL; AF077009; AAC35947.1;
InterPro; IPR001451; Hexapep_transf.
Pfam; PF00132; hexapep, E.ransf.
Transferase; Acyltransferase.
SEQUENCE 354 AA; 38493 MW; 7972D0C013233EF9 CRC64;
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STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 16; Length 354; Pred. No. 34;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UDP-3-O-[3-HYDROXYMYRISTOYL] GLUCOSAMINE N-ACYLLTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40, DB 2; Length 354;
Pred. No. 34;
2; Mismatches 3; Indels
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Pfam: PF00132; hexapep; 8.
Transferase; Acyltransferase; Complete proteome.
SEQUENCE 354 AA; 38404 WW; B9C547C129AE17BB CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
UDP GLUCOSAMINE N-ACYLTRANSFERASE.
LPXD OR CPN0302 OR CP0456.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>.</u>
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Bacteria; Chlamydiales; Chlamydia.
NCBI_TaxID-813;
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                                                                                          STRAIN=LGV-434;
MEDLINE=99392470; PubMed=10463174;
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Science 282:754-759(1998).
EMBL; AE001297; AAC67836.1; -.
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61.5%;
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Best Local Similarity 61.5
Matches 8; Conservative
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| 178 IIQPGAVIGSCGF 190
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Best Local Similarity
Matches 8; Conserv
                                                                SEQUENCE FROM N.A.
NCBI_TaxID=813;
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MEDLINE-37061201: PubMed-8905231;
MEDLINE-37061201: Notani H., Tanaka A., Asamizu E., Nakamura Y.,
Kanako T., Sato S., Kotani H., Tanaka A., Sasamoto S., Kimura T.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabata S.;
                                                                                                                                                  Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL. AL049826; CAB42725.1;
Hypothetical protein.
SEQUENCE 197 AA; 20317 MW; DCC41852B19B3CFE CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UDP-3-0-[3-HYDROXYMYRISTOYL] GLUCOSAMINE N-ACYLTRANSFERASE LPXD.
                                                                                                                        Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
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Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 197;
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SEQUENCE 265 AA: 29760 MW; 3A344CF7BDC25569 CRC64;
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1-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 29.8 KDA PROTEIN.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
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Pred. No. 19;
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                                                          STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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EMBL; D90908; BAA17739.1; -.
InterPro; IPR001440; TPR.
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54.5%;
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170 ECRKVDGATGF 180
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-!- SIMILARITY: BELONGS TO THE WNT FAMILY.
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                                                                                                                       PROSITE; PS00246; WNT1; 1.
Developmental protein; Glycoprotein.
SEQUENCE 362 AA; 40552 MW; CED90
                            EMBL; AF206500; AAF19840.1;
                                              InterPro; IPR000970; Wht1. Pfam; PF00110; wht; 1. SMART; SM00097; WNT1; 1.
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
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SEQUENCE FROM N.A.
SEALY body formation and expression pattern of genes encoding
"Early body formation and expression pattern of genes encoding
secreted proteins, BDBMP2/4, BbMnt7, and BbMnt8 in lancelets.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-i- FONGTION: PROBABLE DEVELOPMENTAL PROTEIN (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: POSSIBLY SECRETED AND ASSOCIATES WITH THE
EXTRACELLULAR MATRIX (BY SIMILARITY).
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EMBL, AE001615; AAD18451.1; --
EMBL, AP002246; BAA98512.1; --
PHCI-2DPAGE, Q928N6; --
TIGR, CP0456; --
                                                                                                                       MEDILINE-99206606; PubMed-10192388; Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Kalman S., Mitchell W., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
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Branchiostoma.
NCBI_TaxID=7741;
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Pfam; PR00132; hexapep; 8.
Transferase; Acyltransferase; Complete protecome.
SEQUENCE 360 AA; 38846 MW; 4CDD843A6AF77B3F CRC64;
  Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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Nucleic Acids Res. 28:1397-1406(2000)
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                            NCBI_TaxID=83558;
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Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00246; WNT1; 1.
Developmental protein; Glycoprotein.
SEQUENCE 364 AA; 40514 MW; 12C105C3CCD45D60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.0%; Score 40; DB 5; 50.0%; Pred. No. 35;
                                           5,
                                  Score 40; DB 5; Pred. No. 35; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                       46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 15, CTrEMBLrel. 15, ICTEMBLrel. 19, ICTEMBLREL. 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01349; WNTPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000970; Wntl.
Ouery Match
Best Local Similarity 50.0
That 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00097; WNT1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00110; wnt; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |::| | ||||
184 RVCKCHGVSGSC 195
                                                                                                                                                                                                                                                                184 RVCKCHGVSGSC 195
                                                                                                                                                                                                                3 RIVQCRSVEGSC 14
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Best Local Similarity
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